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SEQUENCE LISTING

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(1) GENERAL INFORMATION

- (i) APPLICANT: Coughlin, Shaun R.
Ishihari, Hiroaki
Connolly, Andrew
- (ii) TITLE OF THE INVENTION: Protease-Activated Receptor
3 and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 Page Mill Road
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/208,629
(B) FILING DATE: 08-DEC-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/742,440
(B) FILING DATE: 30-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Catherine M. Polizzi
(B) REGISTRATION NUMBER: 40,130
(C) REFERENCE/DOCKET NUMBER: 220002060310
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 813-5600
(B) TELEFAX: (650) 494-0792
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACTTTGTA	TACTTAACAA	CATCCTGTAG	CCGGGTCTCA	GGACATCAAG	ATGAAAATCC	60
TTATCTTGGT	TGCAGCTGGG	CTGCTGTTTC	TGCCAGTCAC	TGTTTGCCAA	AGTGGCATAA	120
ATGTTTCAGA	CAACTCAGCA	AAGCCAACCT	TAACATTAA	GAGTTTAAAT	GGGGGTCCCC	180
AAAATACCTT	TGAAGAATTC	CCACTTTCTG	ACATAGAGGG	CTGGACAGGA	GCCACCACAA	240
CTATAAAAGC	GGAGTGTCCC	GAGGACAGTA	TTTCAACTCT	CCACGTGAAT	AATGCTACCA	300
TAGGATACCT	GAGAAGTTCC	TTAAGTACCC	AAGTGATACC	TGCCATCTAT	ATCCTGCTGT	360
TTGTGGTTGG	TGTACCATCC	AACATCGTGA	CCCTGTGGAA	ACTCTCCTTA	AGGACCAAAT	420
CCATCAGTCT	GGTCATCTTT	CACACCAACC	TGGCCATCGC	AGATCTCCTT	TTCTGTGTCA	480
CACTGCCATT	TAAGATCGCC	TACCATCTCA	ATGGCAACAA	CTGGGTATTT	GGCGAGGTCA	540
TGTGCCGGAT	CACCACGGTC	GTTTTCTACG	GCAACATGTA	CTGCGCTATC	CTGATCCTCA	600
CTTGTCATGGG	CATCAACCGC	TACCTGGCCA	CGGCTCACCC	TTTCACATAC	CAGAAGCTGC	660
CCAAACGCAG	CTTCTCCTTG	CTCATGTGTG	GCATAGTGTG	GGTCATGGTT	TTCTTATACA	720
TGCTGCCCTT	TGTCATCCTG	AAGCAGGAGT	ACCACCTCGT	CCACTCAGAG	ATCACCACCT	780
GCCACGATGT	CGTCGACGCG	TGCGAGTCCC	CATCATCCTT	CCGATTCTAC	TACTTCGTCT	840
CCTTAGCATT	CTTTGGGTTC	CTCATCCCCT	TTGTGATCAT	CATCTTCTGT	TACACGACTC	900
TCATCCACAA	ACTTAAATCA	AAGGATCGGA	TATGGCTGGG	CTACATCAAG	GCCGTCCTCC	960
TCATCCTTGT	GATTTTCACA	ATTTGCTTTG	CCCCACCAA	CATCATACTC	GTAATCCACC	1020
ATGCCAACTA	CTACTACCAC	AATACCGACA	GCTTGTAATT	TATGTATCTT	ATTGCTCTGT	1080
GCCTGGGGAG	CCTGAATAGC	TGCCTAGATC	CATTCTTTTA	CTTTGTCTATG	TCGAAAGTTG	1140
TAGATCAGCT	TAATCCTTAG	TCGGCAATGG	CAAGACCACT	TTAGAGACCA	AGGAGAGATA	1200
TCTGGGAAGA	CATACATGCT	TGGC				1224

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATATGCTA	ATATTTCTT	TCAATTACAG	GCATAAATGT	TTCAGACAAC	TCAGCAAAGC	60
CAACCTTAAC	TATTAAGAGT	TTTAATGGGG	GTCCCCAAAA	TACCTTTGAA	GAATTCNNNN	120
NNNTACAAC	CTCCATGTGA	ATAATGCTAC	CATGGGATAC	CTGAGAAGTT	CCTTAAGTAC	180
CAAAGTGATA	CCTGCCATCT	ACATCCTGGT	GTTTGTGATT	GGTGTACCAG	CGAACATCGT	240
GACCCTGTGG	AAACTCTCCT	CAAGGACCAA	ATCCATCTGT	CTGGTCATCT	TTACACCAA	300
CCTGGCCATC	GCGGATCTCC	TTTTCTGTGT	CACGCTGCCG	TTTAAGATCN	NCCTACCATC	360
TCAATGGCAA	CAACTGGGTA	TTTGGCGAGG	TCATGTGCCG	GATCACCACG	GTCGTTTTCT	420
ACGGCAACAT	GTA CTGCGCT	ANNNTCCTGA	TCCTCACCTG	CATGGGCATC	AACCGCTACC	480
TGGCCACGGC	TCACCCTTTC	ACATACCAGA	AGCTGCCCAA	ACGCAGCTTC	TCCATGCTCA	540
TGTGTGGCAT	GGTGTGGGTC	ATGGTTTTCT	TATACATGCT	GCCCTTTGTC	ATCCNNNAAG	600
CAGGAGTACC	ACCTCGTCCA	CTCCGAGATC	ACCACCTGCC	ACGATGTCGT	CGACGCGTGC	660
GANTCCCCAT	CATCCTTCCG	ATTCTACTAC	TTCTCTCTCT	TAGCATTCTT	TGGGTTCCCTC	720
ATCCCGTTTG	TGATCATCAT	CTTCTGTTAC	ACGACTCTCA	TCCACAAACT	TAAATCAAAA	780
GATCNGATAT	GGCTGGGCTA	CATCAAGGCC	GTCCTCCTCA	TCCTTG TGAA	TTTCACCATC	840
TGCTTCCCCC	CCACCAAGNN	NNNNGATATC	TGGGAAGACG	TACATGCTTG	GCTGACTTGT	900
GCATGGCACC	ATCAGCTCAA	TTTTTAATTT	TTTAATTTTA	ATTTAATTTA	ATTTTATGTT	960

TTTGAGACAG AGCCTCACTG TGTAGTCCTG GCTGGCCTGG CTGGTTCTCT ATTTAGACCA	1020
GGTTAGCCTT GAACTCACAG AGATCTGCCT GCTTCTGCCT CCCAAGTGCT GGGTTCAACC	1080
AGGTCTGGCA AGCGCTCCAT TTTTCAGCTC CTCTGCAACA GTGC	1124

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 5, 386, 394
- (D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr	Leu	Tyr	Thr	Xaa	Gln	His	Pro	Val	Ala	Gly	Ser	Gln	Asp	Ile	Lys
1				5					10					15	
Met	Lys	Ile	Leu	Ile	Leu	Val	Ala	Ala	Gly	Leu	Leu	Phe	Leu	Pro	Val
		20						25					30		
Thr	Val	Cys	Gln	Ser	Gly	Ile	Asn	Val	Ser	Asp	Asn	Ser	Ala	Lys	Pro
	35					40						45			
Thr	Leu	Thr	Ile	Lys	Ser	Phe	Asn	Gly	Gly	Pro	Gln	Asn	Thr	Phe	Glu
	50					55				60					
Glu	Phe	Pro	Leu	Ser	Asp	Ile	Glu	Gly	Trp	Thr	Gly	Ala	Thr	Thr	Thr
65					70				75					80	
Ile	Lys	Ala	Glu	Cys	Pro	Glu	Asp	Ser	Ile	Ser	Thr	Leu	His	Val	Asn
			85						90				95		
Asn	Ala	Thr	Ile	Gly	Tyr	Leu	Arg	Ser	Ser	Leu	Ser	Thr	Gln	Val	Ile
	100						105						110		
Pro	Ala	Ile	Tyr	Ile	Leu	Leu	Phe	Val	Val	Gly	Val	Pro	Ser	Asn	Ile
	115						120					125			
Val	Thr	Leu	Trp	Lys	Leu	Ser	Leu	Arg	Thr	Lys	Ser	Ile	Ser	Leu	Val
	130					135					140				
Ile	Phe	His	Thr	Asn	Leu	Ala	Ile	Ala	Asp	Leu	Leu	Phe	Cys	Val	Thr
145					150				155					160	
Leu	Pro	Phe	Lys	Ile	Ala	Tyr	His	Leu	Asn	Gly	Asn	Asn	Trp	Val	Phe
			165						170				175		
Gly	Glu	Val	Met	Cys	Arg	Ile	Thr	Thr	Val	Val	Phe	Tyr	Gly	Asn	Met
	180						185					190			
Tyr	Cys	Ala	Ile	Leu	Ile	Leu	Thr	Cys	Met	Gly	Ile	Asn	Arg	Tyr	Leu
	195						200					205			
Ala	Thr	Ala	His	Pro	Phe	Thr	Tyr	Gln	Lys	Leu	Pro	Lys	Arg	Ser	Phe
	210					215					220				
Ser	Leu	Leu	Met	Cys	Gly	Ile	Val	Trp	Val	Met	Val	Phe	Leu	Tyr	Met
225				230					235					240	
Leu	Pro	Phe	Val	Ile	Leu	Lys	Gln	Glu	Tyr	His	Leu	Val	His	Ser	Glu
			245					250				255			
Ile	Thr	Thr	Cys	His	Asp	Val	Val	Asp	Ala	Cys	Glu	Ser	Pro	Ser	Ser
		260					265					270			
Phe	Arg	Phe	Tyr	Tyr	Phe	Val	Ser	Leu	Ala	Phe	Phe	Gly	Phe	Leu	Ile
	275						280					285			
Pro	Phe	Val	Ile	Ile	Ile	Phe	Cys	Tyr	Thr	Thr	Leu	Ile	His	Lys	Leu

290		295		300
Lys Ser Lys Asp Arg Ile Trp Leu Gly Tyr Ile	Lys Ala Val Leu Leu			
305		310		320
Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Thr Asn Ile Ile Leu				
	325		330	335
Val Ile His His Ala Asn Tyr Tyr Tyr His Asn Thr Asp Ser Leu Tyr				
	340		345	350
Phe Met Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys Leu				
	355		360	365
Asp Pro Phe Leu Tyr Phe Val Met Ser Lys Val Val Asp Gln Leu Asn				
	370		375	380
Pro Xaa Ser Ala Met Ala Arg Pro Leu Xaa Arg Pro Arg Arg Asp Ile				
385		390		400
Trp Glu Asp Ile His Ala Trp				
	405			

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGCTCCATGA	TTTTACAGAT	TTCATAACGT	TTAAGAGACG	GGACTCAGGT	CATCAAAATG	60
AAAGCCCTCA	TCTTTGCAGC	TGCTGGCCTC	CTGCTTCTGT	TGCCCACCTT	TTGTCAGAGT	120
GGCATGGAAA	ATGATACAAA	CAACTTGGCA	AAGCCAACCT	TACCCATTAA	GACCTTTCGT	180
GGAGCTCCCC	CAAATTCTTT	TGAAGAGTTC	CCCTTTTCTG	CCTTGGAAGG	CTGGACAGGA	240
GCCACGATTA	CTGTAAAAAT	TAAGTGCCTT	GAAGAAAGTG	CTTCACATCT	CCATGTGAAA	300
AATGCTACCA	TGGGGTACCT	GACCAGCTCC	TTAAGTACTA	AACTGATACC	TGCCATCTAC	360
CTCCTGGTGT	TTGTAGTTGG	TGTCCCGGCC	AATGCTGTGA	CCCTGTGGAT	GCTTTTCTTC	420
AGGACCAGAT	CCATCTGTAC	CACTGTATTC	TACACCAACC	TGGCCATTGC	AGATTTTCTT	480
TTTTGTGTTA	CATTGCCCTT	TAAGATAGCT	TATCATCTCA	ATGGGAACAA	CTGGGTATTT	540
GGAGAGGTCC	TGTGCCGGGC	CACCACAGTC	ATCTTCTATG	GCAACATGTA	CTGCTCCATT	600
CTGCTCCTTG	CCTGCATCAG	CATCAACCGC	TACCTGGCCA	TCGTCCATCC	TTTCACCTAC	660
CGGGGCCTGC	CCAAGCACAC	CTATGCCTTG	GTAACATGTG	GACTGGTGTG	GGCAACAGTT	720
TTCTTATATA	TGCTGCCATT	TTTCATACTG	AAGCAGGAAT	ATTATCTTGT	TCAGCCAGAC	780
ATCACCACCT	GCCATGATGT	TCACAACACT	TGCGAGTCCT	CATCTCCCTT	CCAACTCTAT	840
TACTTCATCT	CCTTGGCATT	CTTTGGATTG	TTAATTCCAT	TTGTGCTTAT	CATCTACTGC	900
TATGCAGCCA	TCATCCGGAC	ACTTAATGCA	TACGATCATA	GATGGTTGTG	GTATGTTAAG	960
GCGAGTCTCC	TCATCCTTGT	GATTTTTFAC	ATTTGCTTTG	CTCCAAGCAA	TATTATTCTT	1020
ATTATTACAC	ATGCTAATA	CTACTACAAC	AACACTGATG	GCTTATATTT	TATATATCTC	1080
ATAGCTTTGT	GCCTGGGTAG	TCTTAATAGT	TGCTTAGATC	CATTCTTTTA	TTTTCTCATG	1140
TCAAAAACCA	GAAATCACTC	CACTGCTTAC	CTTACAAAAT	AGTGAAATGA	TCTTAGAGAA	1200
CAAGGACAGC	CATCACAGAG	AACG				1224

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAGGCATGG	AAAATGATAC	AAACAACCTTG	GCAAAGCCAA	CCTTACCCAT	TAAGACCTTT	60
CGTGGAGCTC	CCCCAAATTC	TTTTGAAGAG	TTCCCCTTTT	CTGCCTTGGA	AGGCTGGACA	120
GGAGCCACGA	TTACTGTAAA	AATTAAGTGC	CCTGAAGAAA	GTGCTTCACA	TCTCCATGTG	180
AAAAATGCTA	CCATGGGGTA	CCTGACCAGC	TCCTTAAGTA	CTAAACTGAT	ACCTGCCATC	240
TACCTCCTGG	TGTTTGTAGT	TGGTGTCCCG	GCCAATGCTG	TGACCCTGTG	GATGCTTTTC	300
TTCAGGACCA	GATCCATCTG	TACCACTGTA	TTCTACACCA	ACCTGGCCAT	TGCAGATTTT	360
CTTTTTTGTG	TTACATTGCC	CTTTAAGATA	GCTTATCATC	TCAATGGGAA	CAACTGGGTA	420
TTTGGAGAGG	TCCTGTGCCG	GGCCACCACA	GTCATCTTCT	ATGGCAACAT	GTACTGCTCC	480
ATTCTGCTCC	TTGCCTGCAT	CAGCATCAAC	CGCTACCTGG	CCATCGTCCA	TCCTTTCACC	540
TACCGGGGCC	TGCCCAAGCA	CACCTATGCC	TTGGTAACAT	GTGGACTGGT	GTGGGCAACA	600
GTTTTCTTAT	ATATGCTGCC	ATTTTTTCATA	CTGAAGCAGG	AATATTATCT	TGTTTCAGCCA	660
GACATACCA	CCTGCCATGA	TGTTCAACAAC	ACTTGCGAGT	CCTCATCTCC	CTTCCAACCTC	720
TATTACTTCA	TCTCCTTGCC	ATTCTTTGGA	TTCTTAATTC	CATTTGTGCT	TATCATCTAC	780
TGCTATGCAG	CCATCATCCG	GACACTTAAT	GCATACGATC	ATAGATGGTT	GTGGTATGTT	840
AAGGCGAGTC	TCCTCATCCT	TGTGATTTTT	ACCATTTGCT	TTGCTCCAAG	CAATATTATT	900
CTTATTATTC	ACCATGCTAA	CTACTACTAC	AACAACACTG	ATGGCTTATA	TTTTATATAT	960
CTCATAGCTT	TGTGCCTGGG	TAGTCTTAAT	AGTTGCTTAG	ATCCATTCTC	TTATTTTCTC	1020
ATGTCAAAAA	CCAGAAATCA	CTCCACTGCT	TACCTTACAA	AATAGTGAAA	TGATCTTAGA	1080
GAACAAGGAC	AGCCATCACA	GA				1102

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 9, 394, 395
- (D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Ser	Met	Ile	Leu	Gln	Ile	Ser	Xaa	Arg	Leu	Arg	Asp	Gly	Thr	Gln
1				5				10					15		
Val	Ile	Lys	Met	Lys	Ala	Leu	Ile	Phe	Ala	Ala	Ala	Gly	Leu	Leu	Leu
		20						25				30			
Leu	Leu	Pro	Thr	Phe	Cys	Gln	Ser	Gly	Met	Glu	Asn	Asp	Thr	Asn	Asn
		35						40				45			
Leu	Ala	Lys	Pro	Thr	Leu	Pro	Ile	Lys	Thr	Phe	Arg	Gly	Ala	Pro	Pro
		50						55				60			
Asn	Ser	Phe	Glu	Glu	Phe	Pro	Phe	Ser	Ala	Leu	Glu	Gly	Trp	Thr	Gly
65					70					75				80	
Ala	Thr	Ile	Thr	Val	Lys	Ile	Lys	Cys	Pro	Glu	Glu	Ser	Ala	Ser	His
				85					90					95	
Leu	His	Val	Lys	Asn	Ala	Thr	Met	Gly	Tyr	Leu	Thr	Ser	Ser	Leu	Ser
			100					105						110	
Thr	Lys	Leu	Ile	Pro	Ala	Ile	Tyr	Leu	Leu	Val	Phe	Val	Val	Gly	Val
			115					120						125	
Pro	Ala	Asn	Ala	Val	Thr	Leu	Trp	Met	Leu	Phe	Phe	Arg	Thr	Arg	Ser

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130		135		140	
Ile Cys Thr Thr Val Phe Tyr Thr Asn Leu Ala Ile Ala Asp Phe Leu					
145		150		155	160
Phe Cys Val Thr Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn					
	165		170		175
Asn Trp Val Phe Gly Glu Val Leu Cys Arg Ala Thr Thr Val Ile Phe					
	180		185		190
Tyr Gly Asn Met Tyr Cys Ser Ile Leu Leu Leu Ala Cys Ile Ser Ile					
	195		200		205
Asn Arg Tyr Leu Ala Ile Val His Pro Phe Thr Tyr Arg Gly Leu Pro					
210		215		220	
Lys His Thr Tyr Ala Leu Val Thr Cys Gly Leu Val Trp Ala Thr Val					
225		230		235	240
Phe Leu Tyr Met Leu Pro Phe Phe Ile Leu Lys Gln Glu Tyr Tyr Leu					
	245		250		255
Val Gln Pro Asp Ile Thr Thr Cys His Asp Val His Asn Thr Cys Glu					
	260		265		270
Ser Ser Ser Pro Phe Gln Leu Tyr Tyr Phe Ile Ser Leu Ala Phe Phe					
	275		280		285
Gly Phe Leu Ile Pro Phe Val Leu Ile Ile Tyr Cys Tyr Ala Ala Ile					
290		295		300	
Ile Arg Thr Leu Asn Ala Tyr Asp His Arg Trp Leu Trp Tyr Val Lys					
305		310		315	320
Ala Ser Leu Leu Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Ser					
	325		330		335
Asn Ile Ile Leu Ile Ile His His Ala Asn Tyr Tyr Tyr Asn Asn Thr					
	340		345		350
Asp Gly Leu Tyr Phe Ile Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu					
	355		360		365
Asn Ser Cys Leu Asp Pro Phe Leu Tyr Phe Leu Met Ser Lys Thr Arg					
370		375		380	
Asn His Ser Thr Ala Tyr Leu Thr Lys Xaa Xaa Asn Asp Leu Arg Glu					
385		390		395	400
Gln Gly Gln Pro Ser Gln Arg Thr					
	405				

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys		
1	5	10
Gly Pro Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys		
	20	30
Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro		
	35	45
Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser		
	50	60
Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu		

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65					70					75					80
Gln	Lys	Gln	Leu	Pro	Ala	Phe	Ile	Ser	Glu	Asp	Ala	Ser	Gly	Tyr	Leu
				85					90					95	
Thr	Ser	Ser	Trp	Leu	Thr	Leu	Phe	Val	Pro	Ser	Val	Tyr	Thr	Gly	Val
			100					105					110		
Phe	Val	Val	Ser	Leu	Pro	Leu	Asn	Ile	Met	Ala	Ile	Val	Val	Phe	Ile
		115					120					125			
Leu	Lys	Met	Lys	Val	Lys	Lys	Pro	Ala	Val	Val	Tyr	Met	Leu	His	Leu
	130					135					140				
Ala	Thr	Ala	Asp	Val	Leu	Phe	Val	Ser	Val	Leu	Pro	Phe	Lys	Ile	Ser
145					150					155					160
Tyr	Tyr	Phe	Ser	Gly	Ser	Asp	Trp	Gln	Phe	Gly	Ser	Glu	Leu	Cys	Arg
			165					170						175	
Phe	Val	Thr	Ala	Ala	Phe	Tyr	Cys	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu
			180					185					190		
Met	Thr	Val	Ile	Ser	Ile	Asp	Arg	Phe	Leu	Ala	Val	Val	Tyr	Pro	Met
	195						200					205			
Gln	Ser	Leu	Ser	Trp	Arg	Thr	Leu	Gly	Arg	Ala	Ser	Phe	Thr	Cys	Leu
	210					215					220				
Ala	Ile	Trp	Ala	Leu	Ala	Ile	Ala	Gly	Val	Val	Pro	Leu	Val	Leu	Lys
225					230					235					240
Glu	Gln	Thr	Ile	Gln	Val	Pro	Gly	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp
			245					250						255	
Val	Leu	Asn	Glu	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser
		260					265						270		
Ala	Phe	Ser	Ala	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val
	275					280						285			
Cys	Tyr	Val	Ser	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn
	290					295				300					
Arg	Ser	Lys	Lys	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys
305					310					315					320
Ile	Phe	Ile	Ile	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His
			325						330					335	
Tyr	Ser	Phe	Leu	Ser	His	Thr	Ser	Thr	Thr	Glu	Ala	Ala	Tyr	Phe	Ala
			340					345					350		
Tyr	Leu	Leu	Cys	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro
	355					360						365			
Leu	Ile	Tyr	Tyr	Tyr	Ala	Ser	Ser	Glu	Cys	Gln	Arg	Tyr	Val	Tyr	Ser
	370					375					380				
Ile	Leu	Cys	Cys	Lys	Glu	Ser	Ser	Asp	Pro	Ser	Ser	Tyr	Asn	Ser	Ser
385					390					395					400
Gly	Gln	Leu	Met	Ala	Ser	Lys	Met	Asp	Thr	Cys	Ser	Ser	Asn	Leu	Asn
			405						410					415	
Asn	Ser	Ile	Tyr	Lys	Lys	Leu	Leu	Thr							
		420					425								

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Arg	Ser	Pro	Ser	Ala	Ala	Trp	Leu	Leu	Gly	Ala	Ala	Ile	Leu	Leu
1				5					10					15	
Ala	Ala	Ser	Leu	Ser	Cys	Ser	Gly	Thr	Ile	Gln	Gly	Thr	Asn	Arg	Ser
		20					25						30		
Ser	Lys	Gly	Arg	Ser	Leu	Ile	Gly	Lys	Val	Asp	Gly	Thr	Ser	His	Val
	35						40					45			
Thr	Gly	Lys	Gly	Val	Thr	Val	Glu	Thr	Val	Phe	Ser	Val	Asp	Glu	Phe
	50					55					60				
Ser	Ala	Ser	Val	Leu	Thr	Gly	Lys	Leu	Thr	Thr	Val	Phe	Leu	Pro	Ile
65				70						75					80
Val	Tyr	Thr	Ile	Val	Phe	Val	Val	Gly	Leu	Pro	Ser	Asn	Gly	Met	Ala
			85						90					95	
Leu	Trp	Val	Phe	Leu	Phe	Arg	Thr	Lys	Lys	Lys	His	Pro	Ala	Val	Ile
		100						105					110		
Tyr	Met	Ala	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Ser	Val	Ile	Trp	Phe
	115						120					125			
Pro	Leu	Lys	Ile	Ala	Tyr	His	Ile	His	Gly	Asn	Asn	Trp	Ile	Tyr	Gly
	130					135						140			
Glu	Ala	Leu	Cys	Asn	Val	Leu	Ile	Gly	Phe	Phe	Tyr	Gly	Asn	Met	Tyr
145				150						155					160
Cys	Ser	Ile	Leu	Phe	Met	Thr	Cys	Leu	Ser	Val	Gln	Arg	Tyr	Trp	Val
			165						170					175	
Ile	Val	Asn	Pro	Met	Gly	His	Ser	Arg	Lys	Lys	Ala	Asn	Ile	Ala	Ile
		180						185					190		
Gly	Ile	Ser	Leu	Ala	Ile	Trp	Leu	Leu	Ile	Leu	Leu	Val	Thr	Ile	Pro
	195						200					205			
Leu	Tyr	Val	Val	Lys	Gln	Thr	Ile	Phe	Ile	Pro	Ala	Leu	Asn	Ile	Thr
	210					215					220				
Thr	Cys	His	Asp	Val	Leu	Pro	Glu	Gln	Leu	Leu	Val	Gly	Asp	Pro	Phe
225				230						235					240
Leu	Ser	Leu	Ala	Ile	Gly	Val	Phe	Leu	Phe	Pro	Ala	Phe	Leu	Thr	Ala
			245						250					255	
Ser	Ala	Tyr	Val	Leu	Met	Ile	Arg	Met	Leu	Arg	Ser	Ser	Ala	Met	Asp
		260						265					270		
Glu	Asn	Ser	Glu	Lys	Lys	Arg	Lys	Arg	Ala	Ile	Lys	Leu	Ile	Val	Thr
	275						280					285			
Val	Leu	Ala	Met	Tyr	Leu	Ile	Cys	Phe	Thr	Pro	Ser	Asn	Leu	Leu	Leu
	290					295					300				
Val	Val	His	Tyr	Phe	Leu	Ile	Lys	Ser	Gln	Gly	Gln	Ser	His	Val	Tyr
305					310					315					320
Ala	Leu	Tyr	Ile	Val	Ala	Leu	Cys	Leu	Ser	Thr	Leu	Asn	Ser	Cys	Ile
			325						330					335	
Asp	Pro	Phe	Val	Tyr	Tyr	Phe	Val	Ser	His	Asp	Phe	Arg	Asp	His	Ala
		340						345					350		
Lys	Asn	Ala	Leu	Leu	Cys	Arg	Ser	Val	Arg	Thr	Val	Lys	Gln	Met	Gln
	355						360					365			
Val	Ser	Leu	Thr	Ser	Lys	Lys	His	Ser	Arg	Lys	Ser	Ser	Ser	Tyr	Ser
	370					375					380				
Ser	Ser	Ser	Thr	Thr	Val	Lys	Thr	Ser	Tyr						
385					390										

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Phe Glu Glu Ile Pro Glu Glu Tyr Leu Gln
 1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...29
- (D) OTHER INFORMATION: N=Inosine at residues 3, 12, 18, 21, and 24

- (A) NAME/KEY: Other
- (B) LOCATION: 22...27
- (D) OTHER INFORMATION: N=A or C or G or T at residues 22 and 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTNTACATGC TNMACYTNGC NNTNGCNGA

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 6...21
- (D) OTHER INFORMATION: N=Inosine at residue 6, 9, 12, 15, and 21

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 24
- (D) OTHER INFORMATION: N=A or C or G or T at residue 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Tyr Lys Asp Asp Asp
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
1 5 10 15
Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr
20 25 30
Lys Asp Asp Asp Asp Val Glu
35

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Glu Glu Phe Pro
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Thr Pro Lys
1

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Phe Arg Gly Ala Pro
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Phe Arg Gly Ala Pro Pro Asn Ser
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu
1 5 10 15
Phe Pro Phe Ser Ala Leu Glu
20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Leu Pro Ile Lys Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu
 1             5             10             15
Phe Pro Phe Ser Ala Leu Glu
                20

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Leu Pro Ile Xaa Thr Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu
 1             5             10             15
Glu Phe Pro Phe Ser Ala Leu Glu
                20

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Xaa Pro Arg Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu Phe
 1             5             10             15
Pro Phe Ser Ala Leu Glu
                20

```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Pro Ile Lys

1

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Phe Arg Gly Ala Pro Pro Asn Ser

1

5